PCT

RAW SEQUENCE LISTING                          DATE: 07/29/2004
PATENT APPLICATION:  US/10/502,244           TIME: 16:11:53

Input Set : A:\seq_lst_US.txt
Output Set: N:\CRF4\07292004\J502244.raw

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     5  <110>  APPLICANT: Carmeliet, Peter
     6         Moons, Lieve
     9  <120>  TITLE OF INVENTION: A NOVEL TARGET TO INHIBIT ANGIOGENESIS
    13  <130>  FILE REFERENCE: DECLE70.003APC
C-->16  <140>  CURRENT APPLICATION NUMBER: US/10/502,244
C-->16  <141>  CURRENT FILING DATE: 2004-07-22
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    18  <151>  PRIOR FILING DATE: 2002-02-08
    22  <150>  PRIOR APPLICATION NUMBER: EP02077742.1
    24  <151>  PRIOR FILING DATE: 2002-07-09
    28  <150>  PRIOR APPLICATION NUMBER: EP03100148.0
    30  <151>  PRIOR FILING DATE: 2003-01-24
    34  <160>  NUMBER OF SEQ ID NOS: 2
    38  <170>  SOFTWARE: PatentIn version 3.1
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    46  <212>  TYPE: DNA
    48  <213>  ORGANISM: Homo sapiens
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    67  tcc ctg ttg ctg ctg ggg ctg tgc ggg aac tcc ttt tca gga ggg cag      103
    68  Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln
    69              10                  15                  20
    71  cct tca tcc aca gat gct cct aag gct tgg aat tat gaa ttg cct gca      151
    72  Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala
    73          25                  30                  35
    75  aca aat tat gag acc caa gac tcc cat aaa gct gga ccc att ggc att      199
    76  Thr Asn Tyr Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile
    77      40                  45                  50
    79  ctc ttt gaa cta gtg cat atc ttt ctc tat gtg gta cag ccg cgt gat      247
    80  Leu Phe Glu Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp
    81  55                  60                  65                  70
    83  ttc cca gaa gat act ttg aga aaa ttc tta cag aag gca tat gaa tcc      295
    84  Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser
    85                  75                  80                  85
    87  aaa att gat tat gac aag cca gaa act gta atc tta ggt cta aag att      343
    88  Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val Ile Leu Gly Leu Lys Ile
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89          90              95                  100
91 gtc tac tat gaa gca ggg att att cta tgc tgt gtc ctg ggg ctg ctg     391
92 Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu
93          105             110                 115
95 ttt att att ctg atg cct ctg gtg ggg tat ttc ttt tgt atg tgt cgt     439
96 Phe Ile Ile Leu Met Pro Leu Val Gly Tyr Phe Phe Cys Met Cys Arg
97     120             125             130
99 tgc tgt aac aaa tgt ggt gga gaa atg cac cag cga cag aag gaa aat     487
100 Cys Cys Asn Lys Cys Gly Gly Glu Met His Gln Arg Gln Lys Glu Asn
101 135             140                 145                 150
103 ggg ccc ttc ctg agg aaa tgc ttt gca atc tcc ctg ttg gtg att tgt     535
104 Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile Ser Leu Leu Val Ile Cys
105             155                 160                 165
107 ata ata ata agc att ggc atc ttc tat ggt ttt gtg gca aat cac cag     583
108 Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly Phe Val Ala Asn His Gln
109             170                 175                 180
111 gta aga acc cgg atc aaa agg agt cgg aaa ctg gca gat agc aat ttc     631
112 Val Arg Thr Arg Ile Lys Arg Ser Arg Lys Leu Ala Asp Ser Asn Phe
113         185                 190                 195
115 aag gac ttg cga act ctc ttg aat gaa act cca gag caa atc aaa tat     679
116 Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr Pro Glu Gln Ile Lys Tyr
117     200             205                 210
119 ata ttg gcc cag tac aac act acc aag gac aag gcg ttc aca gat ctg     727
120 Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp Lys Ala Phe Thr Asp Leu
121 215             220                 225                 230
123 aac agt atc aat tca gtg cta gga ggc gga att ctt gac cga ctg aga     775
124 Asn Ser Ile Asn Ser Val Leu Gly Gly Gly Ile Leu Asp Arg Leu Arg
125             235                 240                 245
127 ccc aac atc atc cct gtt ctt gat gag att aag tcc atg gca aca gcg     823
128 Pro Asn Ile Ile Pro Val Leu Asp Glu Ile Lys Ser Met Ala Thr Ala
129             250                 255                 260
131 atc aag gag acc aaa gag gcg ttg gag aac atg aac agc acc ttg aag     871
132 Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys
133     265             270                 275
135 agc ttg cac caa caa agt aca cag ctt agc agc agt ctg acc agc gtg     919
136 Ser Leu His Gln Gln Ser Thr Gln Leu Ser Ser Ser Leu Thr Ser Val
137     280             285                 290
139 aaa act agc ctg cgg tca tct ctc aat gac cct ctg tgc ttg gtg cat     967
140 Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp Pro Leu Cys Leu Val His
141 295             300                 305                 310
143 cca tca agt gaa acc tgc aac agc atc aga ttg tct cta agc cag ctg     1015
144 Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu
145             315                 320                 325
147 aat agc aac cct gaa ctg agg cag ctt cca ccc gtg gat gca gaa ctt     1063
148 Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu
149             330                 335                 340
151 gac aac gtt aat aac gtt ctt agg aca gat ttg gat ggc ctg gtc caa     1111
152 Asp Asn Val Asn Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln
153         345                 350                 355
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155 cag ggc tat caa tcc ctt aat gat ata cct gac aga gta caa cgc caa    1159
156 Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln
157     360                 365                 370
159 acc acg act gtc gta gca ggt atc aaa agg gtc ttg aat tcc att ggt    1207
160 Thr Thr Thr Val Val Ala Gly Ile Lys Arg Val Leu Asn Ser Ile Gly
161 375                 380                 385                 390
163 tca gat atc gac aat gta act cag cgt ctt cct att cag gat ata ctc    1255
164 Ser Asp Ile Asp Asn Val Thr Gln Arg Leu Pro Ile Gln Asp Ile Leu
165                 395                 400                 405
167 tca gca ttc tct gtt tat gtt aat aac act gaa agt tac atc cac aga    1303
168 Ser Ala Phe Ser Val Tyr Val Asn Asn Thr Glu Ser Tyr Ile His Arg
169         410                 415                 420
171 aat tta cct aca ttg gaa gag tat gat tca tac tgg tgg ctg ggt ggc    1351
172 Asn Leu Pro Thr Leu Glu Glu Tyr Asp Ser Tyr Trp Trp Leu Gly Gly
173         425                 430                 435
175 ctg gtc atc tgc tct ctg ctg acc ctc atc gtg att ttt tac tac ctg    1399
176 Leu Val Ile Cys Ser Leu Leu Thr Leu Ile Val Ile Phe Tyr Tyr Leu
177     440                 445                 450
179 ggc tta ctg tgt ggc gtg tgc ggc tat gac agg cat gcc acc ccg acc    1447
180 Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp Arg His Ala Thr Pro Thr
181 455                 460                 465                 470
183 acc cga ggc tgt gtc tcc aac acc gga ggc gtc ttc ctc atg gtt gga    1495
184 Thr Arg Gly Cys Val Ser Asn Thr Gly Gly Val Phe Leu Met Val Gly
185                 475                 480                 485
187 gtt gga tta agt ttc ctc ttt tgc tgg ata ttg atg atc att gtg gtt    1543
188 Val Gly Leu Ser Phe Leu Phe Cys Trp Ile Leu Met Ile Ile Val Val
189         490                 495                 500
191 ctt acc ttt gtc ttt ggt gca aat gtg gaa aaa ctg atc tgt gaa cct    1591
192 Leu Thr Phe Val Phe Gly Ala Asn Val Glu Lys Leu Ile Cys Glu Pro
193     505                 510                 515
195 tac acg agc aag gaa tta ttc cgg gtt ttg gat aca ccc tac tta cta    1639
196 Tyr Thr Ser Lys Glu Leu Phe Arg Val Leu Asp Thr Pro Tyr Leu Leu
197     520                 525                 530
199 aat gaa gac tgg gaa tac tat ctc tct ggg aag cta ttt aat aaa tca    1687
200 Asn Glu Asp Trp Glu Tyr Tyr Leu Ser Gly Lys Leu Phe Asn Lys Ser
201 535                 540                 545                 550
203 aaa atg aag ctc act ttt gaa caa gtt tac agt gac tgc aaa aaa aat    1735
204 Lys Met Lys Leu Thr Phe Glu Gln Val Tyr Ser Asp Cys Lys Lys Asn
205                 555                 560                 565
207 aga ggc act tac ggc act ctt cac ctg cag aac agc ttc aat atc agt    1783
208 Arg Gly Thr Tyr Gly Thr Leu His Leu Gln Asn Ser Phe Asn Ile Ser
209                 570                 575                 580
211 gaa cat ctc aac att aat gag cat act gga agc ata agc agt gaa ttg    1831
212 Glu His Leu Asn Ile Asn Glu His Thr Gly Ser Ile Ser Ser Glu Leu
213         585                 590                 595
215 gaa agt ctg aag gta aat ctt aat atc ttt ctg ttg ggt gca gca gga    1879
216 Glu Ser Leu Lys Val Asn Leu Asn Ile Phe Leu Leu Gly Ala Ala Gly
217     600                 605                 610
219 aga aaa aac ctt cag gat ttt gct gct tgt gga ata gac aga atg aat    1927
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220 Arg Lys Asn Leu Gln Asp Phe Ala Ala Cys Gly Ile Asp Arg Met Asn
221 615                 620                 625                 630
223 tat gac agc tac ttg gct cag act ggt aaa tcc ccc gca gga gtg aat     1975
224 Tyr Asp Ser Tyr Leu Ala Gln Thr Gly Lys Ser Pro Ala Gly Val Asn
225                 635                 640                 645
227 ctt tta tca ttt gca tat gat cta gaa gca aaa gca aac agt ttg ccc     2023
228 Leu Leu Ser Phe Ala Tyr Asp Leu Glu Ala Lys Ala Asn Ser Leu Pro
229                 650                 655                 660
231 cca gga aat ttg agg aac tcc ctg aaa aga gat gca caa act att aaa     2071
232 Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys
233                 665                 670                 675
235 aca att cac cag caa cga gtc ctt cct ata gaa caa tca ctg agc act     2119
236 Thr Ile His Gln Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr
237         680                 685                 690
239 cta tac caa agc gtc aag ata ctt caa cgc aca ggg aat gga ttg ttg     2167
240 Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu
241 695                 700                 705                 710
243 gag aga gta act agg att cta gct tct ctg gat ttt gct cag aac ttc     2215
244 Glu Arg Val Thr Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe
245                 715                 720                 725
247 atc aca aac aat act tcc tct gtt att att gag gaa act aag aag tat     2263
248 Ile Thr Asn Asn Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr
249                 730                 735                 740
251 ggg aga aca ata ata gga tat ttt gaa cat tat ctg cag tgg atc gag     2311
252 Gly Arg Thr Ile Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu
253                 745                 750                 755
255 ttc tct atc agt gag aaa gtg gca tcg tgc aaa cct gtg gcc acc gct     2359
256 Phe Ser Ile Ser Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala
257         760                 765                 770
259 cta gat act gct gtt gat gtc ttt ctg tgt agc tac att atc gac ccc     2407
260 Leu Asp Thr Ala Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro
261 775                 780                 785                 790
263 ttg aat ttg ttt tgg ttt ggc ata gga aaa gct act gta ttt tta ctt     2455
264 Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu
265                 795                 800                 805
267 ccg gct cta att ttt gcg gta aaa ctg gct aag tac tat cgt cga atg     2503
268 Pro Ala Leu Ile Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met
269                 810                 815                 820
271 gat tcg gag gac gtg tac gat gat gtt gaa act ata ccc atg aaa aat     2551
272 Asp Ser Glu Asp Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn
273         825                 830                 835
275 atg gaa aat ggt aat aat ggt tat cat aaa gat cat gta tat ggt att     2599
276 Met Glu Asn Gly Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile
277         840                 845                 850
279 cac aat cct gtt atg aca agc cca tca caa cat tga tagctgatgt          2645
280 His Asn Pro Val Met Thr Ser Pro Ser Gln His
281 855                 860                 865
283 tgaaactgct tgagcatcag gatactcaaa gtggaaagga tcacagattt ttggtagttt   2705
285 ctgggtctac aaggactttc caaatccagg agcaacgcca gtggcaacgt agtgactcag   2765
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291 ttgttttttta cttttttaca ctgagtttct atttagacac tacaacatat ggggtgtttg  2945
293 ttcccattgg atgcatttct atcaaaactc tatcaaatgt gatggctaga ttctaacata  3005
295 ttgccatgtg tggagtgtgc tgaacacaca ccagtttaca ggaaagatgc attttgtgta  3065
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301 atccattttc actaaaagtg tgtgaaacct acagcatatt cttcacgcag agattttcat  3245
303 ctattatact ttatcaaaga ttggccatgt tccacttgga aatggcatgc aaaagccatc  3305
305 atagagaaac ctgcgtaact ccatctgaca aattcaaaag agagagagag atcttgagag  3365
307 agaaatgctg ttcgttcaaa agtggagttg tttttaacaga tgccaattac ggtgtacagt  3425
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313 agatctggtg tccagcatgg atgaaacctt tgagtttggt ccctaaattt gcatgaaagc  3605
315 acaaggtaaa tattcatttg cttcaggagt ttcatgttgg atctgtcatt atcaaaagtg  3665
317 atcagcaatg aagaactggt cggacaaaat ttaacgttga tgtaatggaa ttccagatgt  3725
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341             20                  25                  30
344 Asn Tyr Glu Leu Pro Ala Thr Asn Tyr Glu Thr Gln Asp Ser His Lys
345         35                  40                  45
348 Ala Gly Pro Ile Gly Ile Leu Phe Glu Leu Val His Ile Phe Leu Tyr
349     50                  55                  60
352 Val Val Gln Pro Arg Asp Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu
353 65                  70                  75                  80
356 Gln Lys Ala Tyr Glu Ser Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val
357             85                  90                  95
360 Ile Leu Gly Leu Lys Ile Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys
361             100                 105                 110
364 Cys Val Leu Gly Leu Leu Phe Ile Ile Leu Met Pro Leu Val Gly Tyr
365         115                 120                 125
368 Phe Phe Cys Met Cys Arg Cys Cys Asn Lys Cys Gly Gly Glu Met His
369     130                 135                 140
372 Gln Arg Gln Lys Glu Asn Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile
373 145                 150                 155                 160
376 Ser Leu Leu Val Ile Cys Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly
377                 165                 170                 175
380 Phe Val Ala Asn His Gln Val Arg Thr Arg Ile Lys Arg Ser Arg Lys
381             180                 185                 190
384 Leu Ala Asp Ser Asn Phe Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr
385             195                 200                 205
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L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:62 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:58
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